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OM protein - protein search, using sw model
                                                                                                                       \begin{array}{c} \text{GenCore version 4.5} \\ \text{Copyright (c) 1993 - 2000 Compugen Ltd.} \end{array}
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Run on: March 1, 2001, 15:52:21; Search time 170.72 Seconds (without alignments) 25.057 Million cell updates/sec

Title:
Perfect score:
Sequence:

US-09-331-631A-1_COPY_186_248
355
1 KRDPQQREYEDCRRRCEQQE.....MMNPQRGGSGRYEEGEEEQS 63

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	υ	4	ω	N		No.	Result	
73	73	73	73	73	73	73.5	w	74	74	75	75.5	75.5	77	77.5	77.5	77.5	78	79	79	79.5	84	86	92	101	112	114	120	124	Score		
20.6	•	•	•	•	٠	•		•	•	21.1	•	•	•	٠	•	•		•	•	•	•		٠	•	•	•	•	34.9	Match	Query	,
3190	573	568	562	540	407	582	185	1898	1038	1090	834	330	646	911	910	613	1671	919	411.	236	966	1655	810	605	637	588	566	509	Length		
2	Ν	N	2	N	2	2	N	مسو	N	N	2	2	2	N	N	ν	ν	N	2	2	2	Ν	2	2	2	سم	2	2	BB		
T13828	A53234	T26243	T26242	S21825	T02258	B53234	S71512	A45973	T02634	A41696	T42702	T25169	D82493	B34721	A34721	S27770	S71628	A39248	T29475	T01662	S25365	T13998	T44430	S06398	S35221	FWCNAB	S22477	S08059	ID		
CREB-binding prote		-	hypothetical prote	ike	globulin1 - maize	ike	hypothetical prote	chohyalin	rep protein homolo	н		\sim			androgen receptor	hypothetical prote	ς,		hypothetical prote	globulin-1 - maize	protein	termino] 001Vd	obulir	pre	alpha-globulin B p	n precurs	ha-glob	Description		

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30
68	68	68.5	68.5	69	69	69	69	69	69	70.5	70.5	71	71	71	71.5
19.2	19.2	19.3	19.3	19.4	19.4	19.4	19.4	19.4	19.4	19.9	19.9	20.0	20.0	20.0	20.1
1154	1069	758	679	1023	449	449	448	410	133	1344	447	625	162	139	669
2	N	2	N	2	N	N	N	2	2	2	N	N	Ν	N	2
S69206	T00377	S54522	B75262	S12519	A39692	A38080	S33926	JC5046	I51960	T42637	S52391	A34615	S49259	A26892	JC5662
regulator protein	KIAA0642 protein -	hypothetical prote	conserved hypothet	glutactin - fruit	Wilms' tumor prote	Wilms tumor suscep	Wilms' tumor prote	Wilms' tumor suppr	WT1 zinc-finger ho	hypothetical prote	centrosomin B - mo	profilaggrin – rat	albumin 4 - easter	Mopa box protein -	hepatoma-derived g

ALIGNMENTS

RESULT 2 \$22477 vicilin precursor - cacao (cacao) C;Species: Theobroma cacao (cacao) C;Date: 30-Sep-1993 *text_change 17-Mar-C;Accession: \$22477; \$22478; \$18105; \$22050 R;McHenry, L.; Fritz, p.J. Plant Mol. Biol. 18, 1173-1176, 1992 A;Title: Comparison of the structure and nucleotide sequence of vicilin A;Reference number: \$22477; MUID:92288309 A;Accession: \$22477 A;Molecule type: DNA A;Residues: 1-566 <mch> A;Cross-references: EMBL:X62625 A;Cross-references: EMBL:X62626 C;Genetics: A;Introns: 21171; 269/3; 296/3; 391/3; 502/1 C;Superfamily: 9lycinin</mch>	Query Match 34.9%; Score 124; DB 2; Length 509; Best Local Similarity 37.0%; Pred. No. 9.1e-06; Matches 34; Conservative 9; Mismatches 15; Indels 34; G Oy 3 DPOQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMM 11:	RESULT 1 \$08059 Alternate names: seed storage protein C; Species: Gossypium hirsutum (upland cotton) C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep C; Accession: \$08059 R; Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 A; Title: Developmental biochemistry of cottonseed embryogenesis and ge A; Reference number: \$06398 A; Status: not compared with conceptual translation A; Molecule type: DNA A; Residues: 1-509 <chl> C; Superfamily: glycinin</chl>
7-маr-1999 icilin genes of coco	4; Gaps 5; мм 45 QRPEK 59	ment) 30-Sep-1993 and germination. XIX.

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A;Experimental Source: var. Coker 201

R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.

Plant Mol. Biol. 9, 533-546, 1987

A;Pitle: Developmental biochemistry of cottonseed embryogenesis

A;Reference number: S06398

A;Accession: S06911

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein.

C;Superfamily: glycinin

C;Superfamily: glycinin; seed: storage protein

F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status prediction

F;417/Binding site: carbohydrate (Asn) (covalent) #status prediction
                                                                                          globulin Beg1 precursor - barley
C;Species: Hordeum vulgare (barley)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
                                                                                                                                                           RESULT
S35221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-globulin B precursor (clone C72) - upland cotton RyAlternate names: seed storage protein; vicilin precursor C:Species: Gossypium hirsutumu (upland cotton) C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change C:Accession: A30838; S06911
R:Chlan, C.A.: Pyle, J.B.: Legocki, A.B.: Dure III, L. Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis
Mol. Gen. Genet. 239, 209-218, 1993
A;Title: Barley embryo globulin 1 gene, B
A;Reference number: S35221; MUID:93287988
                                                        C; Accession: S35221
R; Heck, G.R.; Chamberlain, A.K.;
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A;Experimental source: var. Coker 201
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A; Residues: 1-588 < CHL>
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                                                                                                                                                                                                                                                                                                                                          DPQQREYEDCRRRCEQQEPRQQHQCQLRC----REQQ-----
                                                                                                                                                                                                                                        KQQCVRECRERYQENPWRREREEEAEEEETEEGEQEQS
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                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%;
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No. 0.00012;
                    Beg1:
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?.6e-05;
                      characterization
                                                                                                                                                                                                                                          178
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C;Genetics:
A;Gene: Beg1
A;Map position: 4
C;Superfamily: glyclnin
C;Keywords: glycoprotein
F;174-190/Product: globulin B
                                                                                         R:Yamada, K.; Shimada, T.; Kondo, M.; Nish
J. Biol. Chem. 274, 2563-2570, 1999
A:Title: Multiple functional proteins are
A:Reference number: Z22767; MUID:99107919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Gossypium hirsutum (upland cotton)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C:Accession: S06398
R:Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Status: preliminary; 1
A;Molecule type: mRNA
A;Residues: 1-810 <YAM>
A;Cross-references: EMBJ
                                                                                                                                                               protein PV100 [imported] - winter squash
C;Species: Cucurbita maxima (winter squash)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T44430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-605 <CHL>
C; Superfamily: glycinin
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A;Status: not compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S35221
A; Molecule type: mRNA
A; Residues: 1-637 <HEC>
                                                                       A; Accession: T44430
                                                                                                                                                                                                                                              T44430
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                                                                                                                                                                                                                                                                                                                                                                                                                            3 DPQQREYEDCRRRCEQQEPRQQHQCQLRCREQ-QRQHGRGGDMM---
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26; Conservative
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 EMBL: AB019195; NID: g3808061; PIDN: BAA34056.1;
                                                        translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                      - NPORG-GSGRYEEGEEEQS
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                                                                                                                                               M.; Nishimura, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 2; Pred. No. 0.0027;
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PID:93808062
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R:Feldmann, H.; Mannhaupt, G.; Sch
submitted to the Protein Sequence
A;Reference number: $45927
A;Accession: $45980
                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-966 <MAND
A;Cross-references: EMBL:X66247; NID:g3548; PIDN:CAA46973.1; PID:g3550
A;Cross-references: EMBL:X66247; NID:g3548; PIDN:CAA46973.1; PID:g3550
A;Cross-references: Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the right arm of yeast chromosor
A;Reference number: $48255; MUID:95208357
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 8, 397-408, 1992
A;Title: Molecular analysis
A;Reference number: S25364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: Z17850; MUID:94365848
A;Accession: T13998
A;Status. -----
                                                                                                          A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55615.1; A;Note: the nucleotide sequence was submitted to the EMBL Data R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I. submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000 C;Accession: S25365; S48277; S45980; S25404; S25405; A30906; S44692 R;Mannhaupt, G; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H. Yeast 8, 397-408, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
C;Accession: T13998
    A; Molecule type: DNA
A; Residues: 1-966 <F
A; Cross-references: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYC8 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: glucose repression mediator; protein YBR0908; protein YBR112c; C;Species: Saccharomyces cerevisiae
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                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; translation not
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A; Residues: 1-1655 < NEW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene mastermind protein - fruit fly (Drosophila virilis)
C; Species: Drosophila virilis
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Best Local Similarity 32.8
Matches 19; Conservative
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                      1-966 <FE2>
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    EMBL: 235981;
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    NID: g536449;
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Pred. No. 0.031;
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Pred. No. 0.25;
6; Mismatches 1
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PIDN:CAA85069.1; PID:g536450; MIPS:YBR112d
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Library, April 1994
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  hypothetical protein
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R;Hilton, H.; Gaut, B.S.
Genetics 150, 863-872, 1998
A;Title: Speciation and domestication in maize
A;Reference number: Z14386; MUID:98429537
A;Accession: T01662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: unassigned tetratricopeptide repeat p
C;Keywords: nucleus; transcription regulation
F;224-257/Domain: tetratricopeptide repeat homology
F;262-295/Domain: tetratricopeptide repeat homology
F;296-329/Domain: tetratricopeptide repeat homology
F;330-363/Domain: tetratricopeptide repeat homology
F;365-398/Domain: tetratricopeptide repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Zea mays (maize)
C;Date: 19-reb-1999 #sequence_revision 19-Feb-1999
                                                                                                                                                                            C; Superfamily: glycinin
                                                                                                                                                                                                   A; Introns:
                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-236 <HIL>
A;Cross-references: EMBL:AF064222; NID:g3414836; PIDN:AAC31465.1; PID:g3414837
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A;Map position: 2R
C;Function:
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A;Residues: 1-546,'K',548-966 <TRU>
A;Cross-references: EMBL:M23440; NID:g171349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Trumbly, R.J.
Gene 73, 97-111, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schultz, J.; Carlson, M.
Mol. Cell. Biol. 7, 3637-3645, 1987
A;Title: Molecular analysis of SSNG, a gene functionally related
A;Reference number: S25404; MUID:88065502
                                                                                                                                                                                                                                      A; Experimental source: subspecies
                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SGD:CYC8; SSN6; CRT8
A;Cross-references: SGD:S0000316; MIPS:YBR112c
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A; Residues: 1-546, 'K', 548-966 <SCH>
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                                                                                                Query Match
Best Local (
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Best Local
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                                    12 CRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ
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  CVRRCEDRPWHQRPRCLEQCREEERSRHEADD
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                                                                            17; Conservative
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17; Consert
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                                                                            Score 79.5; I
Pred. No. 0.21
8; Mismatches
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Pred. No. 0.25;
5; Mismatches
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-RSGEGSSEDERERK 85
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T01D1.6

Caenorhabditis elegans

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A; Molecule type: DNA
A; Residues: 1-919 <LUB>
A; Residues: 1-919 <LUB>
A; Residues: 1-919 <LUB>
A; Cross-references: GB:M27423; GB:M27430; NID:g178904; PIDN:AAA51886.1; PID:g178906
A; Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkmann Mol. Cell. Endocrinol. 61, 257-262, 1989
A; Title: "The N-terminal domain of the human androgen receptor is encoded by one, large A; Reference number: A30328; MUID:89137730
A; Accession: A30328
                                                                                                                                               A;Cross-references: GB:M20132
R;Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.;
J. Mol. Endocrinol. 2, R1-R4, 1989
A;Title: Structural organization of the human androgen receptor gene.
A;Reference number: A60946; MUID:89322749
A;Accession: A60946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Homo sapiens (man)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C:Accession: A39248; A30328; A40109; A60946; A34942; A27653; A40108; A40494; A32224; A40
R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, E.M.; Fr
Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989
A:Title: Sequence of the intron/exon junctions of the coding region of the human androge A; Reference number: A39248; MUID:90083302
A:Accession: A39248
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 559-624 <LU2>
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Cloning of human androgen receptor complementary DNA and localization A; Reference number: A40109; MUID:88178112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-77,79-165,'A',167-389,'L',391-464,473-538 <FAB>
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A; Introns: 25/3; 304/3
C; Superfamily: gliadin
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A; Residues: 1-411 <BRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 240, 327-330, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Lubahn,
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                                                                Lubahn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Caenorhabditis elegans; Species: Caenorhabditis elegans; Species: Caenorhabditis elegans; Species: Caenorhabditis elegans; Species: Caenorhabditis elegans
                                                                                              Residues:
                                                                                                                       Molecule type: DNA
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Best Local
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                                    Endocrinol.
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                                                             D.B.; Joseph,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Wilson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQREYEDCRRRC-EQQEPRQ--QHQCQLRCRE------
                        536-540;587-591;626-631;723-726;770-774;814-818;867-870 <KUI>
B.; Joseph, D.R.; Sar, M.; Tan, J.; Higgs, H.N.; Larson, R.E.; French, [nol. 2, 1265-1275, 1988]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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   androgen
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receptor: complementary
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    QQRQHGRGGDMMNPQRGGS 52

deoxyribonucleic
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A;Introns: 538/2; 589/1; 628/1; 724/1; 772/2; 816/1; 868/3
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology C;Keywords: DNA binding; steroid binding; transcription regulation; zinc finger F;557-815/Domain: erbA transforming protein homology <ERBA>
F;559-579/Region: zinc finger
F;595-619/Region: zinc finger
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A; Molecule type: mRNA
A; Residues: 468-564, 'K', 566-919 <TRA>
A; Residues: 468-564, 'K', 566-919 <TRA>
A; Cross-references: GB:M20260; NID:9178891; PIDN:AAA51774.1; PID:9178892
A; Note: the authors translated the codon AAG for residue 565 as Glu
A; Note: \( \text{Note} \), \( \text{Kontis} \), \( \text{Liao} \), \( \text{S} \).
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A; Residues: 1-77, 79-211, 'R', 213-471,473-919 <TIL>
A; Cross-references: GB:M21748; GB:J04150; NID:g178871;
R; MOWSZOWICZ, I; Lee, H.J.; Chen, H.T.; Mestayer, C.;
Mol. Endocrinol. 7, 861-869, 1993
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Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988
A;Title: Structural analysis of complementary DNA
A;Reference number: A40494; MUID:89017168
A;Accession: A40494
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Science 240, 324-326, 1988
A;Title: Molecular cloning of human and rat complementary
A;Reference number: A40108; MUID:88178111
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A;Cross-references: GB.M20132; NID:g178627; PIDN:AAA51729.1; PID:g178628; GB:J03180
A;Trapman, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.;
Biochem. Biophys. Res. Commun. 153, 241-248, 1988
A;Title: Cloning, structure and expression of a cDNA encoding the human androgen rece
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A;Residues: 557-614,'H',616-624 <MOW>
A;Cross-references: PIDN:AAB28340.1; PID:g425580
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A; Residues: 557-628 < CHA>
A; Cross-references: GB: M18624
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A; Residues: 1-74,79-89,'H',90-472,'GGG',473-474,'E',476-644,'N',646-919
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A; Residues: 1-919 < LU
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A;Accession: A34942
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Best Local Similarity
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    58
                                                                                       5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ
QQQQQQ--QQQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ
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32.8%;
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Pred. No.
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                                                                                                                                                                                    Indels
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                                                                                                                                                                                    Gaps
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sensory transduction hist C; Species: Dictyostelium

histidine kina lium discoideum

kinase

doka -

slime

mold

(Dictyostelium

discoideum)

RESULT

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C;Accession: S27770
R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H. submitted to the EMBL Data Library, June 1992
A;Description: Distinct families of site-specific retroposons occu
                                                              В
                                                                                                      20
                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 1 - African malaria mosquito (fragment) C:Species: Anopheles gambiae (African malaria mosquito) C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_charc: Accession: $27770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: dokA
C; Function:
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A;Residues: 1-149,'E',151-219,'TRYLKLIQSTNNWTYWY',238-1671 <SCW>
A;Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; PID:e233513; PID:g123720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain AX2; substrain 214 R;Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, submitted to the EMBL Data Library, March 1996 A;Description: The hybrid histidine kinase Doka is F
RESULT
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A; Residues: 1-613 <BES>
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A;Accession: S71628
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A:Accession: S78068
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C; Accession:
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Best Local S
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Best Local :
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                                                                                                                                                  245 QQQQQQQQRNQQREWQQQQQQQQQHQQREQQQQQRVQQQNQQHQRQQQQQQQQQQR----QQ 300
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                                                              301 QQQQEQQ 307
                                                                                                                                                                                                                                          Local Similarity 28.4 nes 19; Conservative
                                                                                                        56 EEGEEEQ 62
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sion: S71628; S78068
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27.8%;
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                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                          Score 77.5; DB Pred. No. 0.78; 7; Mismatches
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Search completed: March Job time: 547 sec

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F;550-570/Region: zinc finger
F;586-610/Region: zinc finger
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R; Govindan, M.V.
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A; Title: Specific region in hormone binding domain A; Reference number: A34721; MUID:90258935
A; Accession: A34721
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C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
C:Accession: A34721
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A; Residues: 1-911 <GO2>
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C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
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C;Keywords: zinc finger
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A; Residues: 1-910 <GOV>
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Best Local Similarity
Matches 19; Conserv
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                                                                                                 Query Match
Best Local Similarity
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58 QQQQQQ----QQQQQQQQQQQQQQETSPRQQQQQQGEDGSPQAHRRGPTGYLVLDEEQQ 112
                                        5 QQREYEDCRRRCEQQEPRQQHQCQLRCREQQRQHGRGGDMMNPQRGGSGRYEEGEEEQ 62
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Pred. No. 1.1;
14; Mismatches
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Pred. No. 1.1;
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